



Sequence Listing US10069427.txt

SEQUENCE LISTING

<110> Famodu, Omolayo O.
Kinney, Anthony J.

<120> Genes Encoding Sterol Delta-14 Reductase in Plants

<130> 2119-4293

<140> 10/069,427
<141>

<150> 60/156,820
<151> 1999-09-30

<160> 10

<170> Microsoft Office 95

<210> 1
<211> 427
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (360)
<223> n=a,c,g or t

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aactccgttc ctttgcttgc ggggttcttc acttacttgg ccgttgcgtgg atccattctc 120
cctggaaaac ttgttcctgg cggtgcacta ctcgatggaa ctcgtctaca ctattgctgc 180
aatggctgc tctcgcttct tctgttgggt gcacttctcg ggatcgggtgc caagatgggt 240
tttgcgtctc ccactgccc atcaaacaga ggacttgagc tgctgtccac aactttgcc 300
ttcagtttc ttgttaaccct gatattgcat ttttccgggt gcaagtacaca aagtaaaggn 360
tcataactaa agcctcatct cagtgggAAC ctgatacacg attgggtgggt tggaaataca 420
actaaaa 427

<210> 2
<211> 126
<212> PRT
<213> Glycine max

<400> 2
Leu Gln Ala Leu Thr Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly
1 5 10 15

Phe Phe Thr Tyr Leu Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu
20 25 30

Val Pro Gly Val Ala Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys
35 40 45

Asn Gly Leu Leu Ser Leu Leu Leu Val Ala Leu Leu Gly Ile Gly
50 55 60

Ala Lys Met Gly Phe Val Ser Pro Thr Ala Ile Ser Asn Arg Gly Leu
65 70 75 80

Glu Leu Leu Ser Thr Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile
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85

90

95

Leu His Phe Ser Gly Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys
 100 105 110

Pro His Leu Ser Gly Asn Leu Ile His Asp Trp Trp Phe Gly
 115 120 125

<210> 3

<211> 667

<212> DNA

<213> Zea mays

<400> 3

ccacgcgtcc ggaagaacaa agtagagctg tccctttgt ctggtctagc taacttatgc 60
 atcttctta ttggctacct agtgttccga ggagctaaca agcaaaaaca tgtgttcaag 120
 aaggacccca aagctcctat atggggaaaa cctcccaaag ttgtcgaaaaaa aaagctacta 180
 gcatctggtt actggggcat cgcaaggcac tgcaattatc tcggagacct gctgctagca 240
 ctttgcgttca gcttgcctt tggagttagt tccgtggtcc catacttcta ccccacgtac 300
 ctgctcattc tactggtctt gagggaaagg cgcgatgagg cgaggtgctc gcagaagttac 360
 agggagatct gggcagagta ctgcaggatc gtggccgttggaa ggatctgttgc ttatgtgtac 420
 tgaagagacg gttagaaacca aggcagctca tggccctggg ccagctgtaa accttatttt 480
 gtttgcctt aaccagtgg tgaatgttga ttagactc ggtttaaactgt gaccgtgcaa 540
 actttgtta ttgttgggtt atacatgttt ggaatcgtga atcagaccgc ctcacttgg 600
 ggcaaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 660
 aaaaaag 667

<210> 4

<211> 140

<212> PRT

<213> Zea mays

<400> 4

Pro Arg Val Arg Lys Asn Lys Val Glu Leu Ser Leu Leu Ser Gly Leu
 1 5 10 15

Ala Asn Leu Cys Ile Phe Leu Ile Gly Tyr Leu Val Phe Arg Gly Ala
 20 25 30

Asn Lys Gln Lys His Val Phe Lys Lys Asp Pro Lys Ala Pro Ile Trp
 35 40 45

Gly Lys Pro Pro Lys Val Val Gly Gly Lys Leu Leu Ala Ser Gly Tyr
 50 55 60

Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Leu Leu Ala
 65 70 75 80

Leu Ser Phe Ser Leu Pro Cys Gly Val Ser Ser Val Val Pro Tyr Phe
 85 90 95

Tyr Pro Thr Tyr Leu Leu Ile Leu Val Leu Arg Glu Arg Arg Asp
 100 105 110

Glu Ala Arg Cys Ser Gln Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Cys
 115 120 125

Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
 130 135 140

<210> 5

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<211> 1631
 <212> DNA
 <213> Glycine max

<400> 5

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tccatcttgg	aactccgttc	cttgcgttgc	ggggttcttc	acttacttgg	ccgttgcgtgg	180
atccattctc	cctggaaaaac	ttgttccctgg	cgttgcacta	ctcgatggaa	ctcgcttaca	240
ctattgctgc	aatggtctgc	tctcgcttct	tctgttgggt	gcacttctcg	ggatcggtgc	300
caagatgggt	tttgtgtctc	ccactgccc	atcagacaga	ggacttgagc	tgctgtccac	360
aactttgcc	ttcagttttc	ttgttaaccct	gatattgcat	tttccgggtt	gcaagtccaca	420
aagtaaaggt	tcatcactaa	agcctcatct	cagtggaaac	ctgatacacg	attggtggtt	480
tggtatacaa	ctaaatccac	agttcatggg	tatcgaccc	aaatttttct	ttgttagagc	540
tggaatgatg	ggatggctac	ttatcaattt	atctatttctt	atgaagagca	ttcaagatgg	600
tactttgagc	cagtcaatga	ttctctacca	gttattctgt	gcactataca	tcctggacta	660
ttttgtacat	gaagagtaca	tgacatccac	ctgggacata	attgcagaga	gactgggctt	720
catgttggtc	tttggagatt	tagtgtggat	tcctttctct	ttcagcatac	aggatgggtg	780
gctcttgatg	aacagtgtgg	agttAACACC	agctgcccatt	gtagctaatt	gttttggtt	840
cctgatttgg	tacatggat	ttcgaggagc	aaacaagcaa	aagcatgtgt	tcaaaaagaa	900
tccaaaggct	cctatctggg	gtaagcctcc	aaaagtattt	gggtggaaagc	tacttgcttc	960
tgttatttgg	gttatttgc	gacatgtaa	ttacacttgg	gatttgatgc	ttgctcttc	1020
ctttagctt	ccatgtggga	taagttacc	aattccatata	ttctatccaa	tttatcttc	1080
tattcttta	atctggagag	agagaaggga	tgaagctcg	tgcggcggaa	agtataagaga	1140
gatatgggccc	gagtatcgta	aacttgcgttcc	atggagaata	ttgccttacg	tttatttagga	1200
tgaaaaaaaaa	aagggttca	ccatgaattt	ttcatcttc	cgatgttatt	aagcaccc	1260
atgttaaattt	gttcttgc	tttgttggttc	aatcttggat	cttttcttat	tgagccatgt	1320
agctgcagga	gagtgtttcg	agggtttat	cttaccatct	atatttgcgt	atcattatgc	1380
tgcagccctgc	aggccctcat	ttttcaatgg	ccaactctt	ttgacttgc	ctattttgtt	1440
tttagatgaga	atttcatgtt	caaagctcct	aggctaaaaa	aaacagtgc	atgttctatg	1500
ggaagtgcag	gaagcaattc	ggggactgca	ggaagcaatt	gcctttacat	tgatatgctc	1560
aatggtactt	taggcctttt	aatgttcttg	cttttcattt	gtgagttatt	attggccccca	1620
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<210> 6
 <211> 374
 <212> PRT
 <213> Glycine max

<400> 6

Met	Met	Glu	Ser	His	Val	Asp	Leu	Gly	Phe	Leu	Leu	Gln	Ala	Leu	Thr
1					5				10				15		

Pro	Ser	Trp	Asn	Ser	Val	Pro	Leu	Leu	Val	Gly	Phe	Phe	Thr	Tyr	Leu
					20				25				30		

Ala	Val	Ala	Gly	Ser	Ile	Leu	Pro	Gly	Lys	Leu	Val	Pro	Gly	Val	Ala
					35			40				45			

Leu	Leu	Asp	Gly	Thr	Arg	Leu	His	Tyr	Cys	Cys	Asn	Gly	Leu	Leu	Ser
					50			55				60			

Leu	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gly	Ile	Gly	Ala	Lys	Met	Gly	Phe
					65			70			75		80		

Val	Ser	Pro	Thr	Ala	Ile	Ser	Asp	Arg	Gly	Leu	Glu	Leu	Leu	Ser	Thr
					85			90					95		

Thr	Phe	Ala	Phe	Ser	Phe	Leu	Val	Thr	Leu	Ile	Leu	His	Phe	Ser	Gly
					100			105				110			

Cys	Lys	Ser	Gln	Ser	Lys	Gly	Ser	Ser	Leu	Lys	Pro	His	Leu	Ser	Gly

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115

120

125

Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
 130 135 140

Met Gly Ile Asp Leu Lys Phe Phe Phe Val Arg Ala Gly Met Met Gly
 145 150 155 160

Trp Leu Leu Ile Asn Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly
 165 170 175

Thr Leu Ser Gln Ser Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr
 180 185 190

Ile Leu Asp Tyr Phe Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp
 195 200 205

Ile Ile Ala Glu Arg Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val
 210 215 220

Trp Ile Pro Phe Ser Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn
 225 230 235 240

Ser Val Glu Leu Thr Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe
 245 250 255

Leu Ile Gly Tyr Met Val Phe Arg Gly Ala Asn Lys Gln Lys His Val
 260 265 270

Phe Lys Lys Asn Pro Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val
 275 280 285

Ile Gly Gly Lys Leu Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His
 290 295 300

Cys Asn Tyr Leu Gly Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro
 305 310 315 320

Cys Gly Ile Ser Ser Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu
 325 330 335

Ile Leu Leu Ile Trp Arg Glu Arg Arg Asp Glu Ala Arg Cys Ala Glu
 340 345 350

Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg
 355 360 365

Ile Leu Pro Tyr Val Tyr
 370

<210> 7
 <211> 1364
 <212> DNA
 <213> Glycine max

<400> 7
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 gtgatgatgg agtcacacgt ggatcttagt tttctcccttc aagctctcac tccatcttgg 120
 aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgcgtgg atccattctc 180
 cctggaaaac ttgttcctgg cgttgcacta ctcgatgaa ctcgtctaca ctattgctgc 240

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aatggctgc	tctcgcttct	tctgtgggt	gcacttcgc	ggatcggtgc	caagatgggt	300
tttggctc	ccactgccc	atcagacaga	ggacttgagc	tgctgtccac	aactttgcc	360
ttcagtttc	ttgttaaccct	gatattgc	ttttccgggtt	gcaagtaca	aagtaaagg	420
tcatcaacta	agcctcactt	cagtggaaac	ctgatacacg	attgggtgggtt	tggtatacaa	480
ctaaatccac	agttcatggg	tatcgacctc	aaagctggaa	tgatgggatg	gctacttata	540
aatttatcta	ttcttatgaa	gagcattcaa	gatggtaactt	tgagccagtc	aatgattctc	600
taccagctat	tctgtgact	atacatcctg	gactattttg	tacatgaaga	gtacatgaca	660
tccacctggg	acataattgc	agagagactg	ggcttcatgt	tggtcttgg	agatttagtg	720
tggattccctt	tctcttcag	catacaggga	tggggctct	tgatgaacag	tgtggagtt	780
acaccagctg	ccattgttagc	taattgctt	gtgttcctga	ttggatacat	ggtatttcga	840
ggagcaaaca	agcaaaaagca	tgtgtcaaa	aagaatccaa	aggctcctat	ctggggtaag	900
cctccaaaag	tcattgggtt	aaagctactt	gcttctgggtt	attggggat	tgctagacac	960
tgttaattacc	taggggattt	gatgcttgct	ctctcctta	gcttaccatg	tgggataagt	1020
tcaccaattc	catacttcta	tccaatttat	cttcttattc	tgttaatctg	gagagagaga	1080
acggatgaag	ctcggtgcgc	cgagaagtat	agagagat	gggcccggat	tcgtaaactt	1140
gttccatgg	aatattgcc	ttacgtttat	taggatgaaa	aaaaaaagg	cttcaccatg	1200
aattcttcat	cttgccatg	ttattaagca	cttcgatgt	aattgggtct	tgttctgt	1260
gttcaatct	tggatcttt	cttattgagc	catgtagctg	caggagatg	tttcgaggga	1320
tttatcttac	catctatatt	tgttaaaaaa	aaaaaaa	aaaa		1364

<210> 8

<211> 369

<212> PRT

<213> Glycine max

<400> 8

Met	Met	Glu	Ser	His	Val	Asp	Leu	Gly	Phe	Leu	Leu	Gln	Ala	Leu	Thr
1					5				10					15	

Pro	Ser	Trp	Asn	Ser	Val	Pro	Leu	Leu	Val	Gly	Phe	Phe	Thr	Tyr	Leu
						20			25				30		

Ala	Val	Ala	Gly	Ser	Ile	Leu	Pro	Gly	Lys	Leu	Val	Pro	Gly	Val	Ala
						35		40			45				

Leu	Leu	Asp	Gly	Thr	Arg	Leu	His	Tyr	Cys	Cys	Asn	Gly	Leu	Leu	Ser
						50		55		60					

Leu	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gly	Ile	Gly	Ala	Lys	Met	Gly	Phe
						65		70		75			80		

Val	Ser	Pro	Thr	Ala	Ile	Ser	Asp	Arg	Gly	Leu	Glu	Leu	Leu	Ser	Thr
						85		90			95				

Thr	Phe	Ala	Phe	Ser	Phe	Leu	Val	Thr	Leu	Ile	Leu	His	Phe	Ser	Gly
						100		105			110				

Cys	Lys	Ser	Gln	Ser	Lys	Gly	Ser	Ser	Leu	Lys	Pro	His	Leu	Ser	Gly
						115		120			125				

Asn	Leu	Ile	His	Asp	Trp	Trp	Phe	Gly	Ile	Gln	Leu	Asn	Pro	Gln	Phe
						130		135			140				

Met	Gly	Ile	Asp	Leu	Lys	Ala	Gly	Met	Met	Gly	Trp	Leu	Leu	Ile	Asn
145						150			155			160			

Leu	Ser	Ile	Leu	Met	Lys	Ser	Ile	Gln	Asp	Gly	Thr	Leu	Ser	Gln	Ser
						165			170		175				

Met	Ile	Leu	Tyr	Gln	Leu	Phe	Cys	Ala	Leu	Tyr	Ile	Leu	Asp	Tyr	Phe
						180		185			190				

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Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg
195 200 205

Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val Trp Ile Pro Phe Ser
210 215 220

Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn Ser Val Glu Leu Thr
225 230 235 240

Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe Leu Ile Gly Tyr Met
245 250 255

Val Phe Arg Gly Ala Asn Lys Gln Lys His Val Phe Lys Lys Asn Pro
260 265 270

Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val Ile Gly Gly Lys Leu
275 280 285

Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly
290 295 300

Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser
305 310 315 320

Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp
325 330 335

Arg Glu Arg Thr Asp Glu Ala Arg Cys Ala Glu Lys Tyr Arg Glu Ile
340 345 350

Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val
355 360 365

Tyr
369

<210> 9
<211> 430
<212> PRT
<213> Ascobolus immersus

<400> 9
Met Gly Gly Lys Asp Tyr Glu Phe Gly Gly Pro Ile Gly Thr Gly Val
1 5 10 15

Leu Met Leu Ile Leu Pro Pro Ile Ser His Tyr Leu His Phe Leu Ile
20 25 30

Thr Pro Arg Gly Ala Pro Pro Pro Glu Phe Trp Ser Ala Pro Leu Glu
35 40 45

Thr Leu Lys Ser Val Thr Pro Thr Phe Ser Ser Leu Phe Ser Leu His
50 55 60

Ala Thr Leu Ala Val Ala Ala Tyr Tyr Leu Leu Leu Val Ala Leu Met
65 70 75 80

Tyr Val Leu Pro Ala Glu Ile Ala Glu Gly Val Val Leu Lys Asp Gly
85 90 95

Ser Arg Leu Lys Tyr Arg Cys Asn Ala Phe Thr Thr Phe Leu Val Phe
100 105 110

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Phe Thr Phe Leu Gly Thr Met Thr Val Leu Glu Gly Pro Thr Trp Trp
115 120 125

Phe Trp Ser Tyr Leu Thr Asp Asn Phe Ala Gln Leu Gln Ser Ala Ser
130 135 140

Ile Val Phe Ser Tyr Ala Met Ser Leu Trp Val Tyr Ile Arg Ser Tyr
145 150 155 160

Arg Pro Met Pro Lys Gly Lys Glu Val Ile Leu Ser Pro Val Gly Phe
165 170 175

Lys Gly Asn His Ile His Asp Phe Trp Met Gly Arg Glu Leu Asn Pro
180 185 190

Arg Ile Gly Glu Trp Leu Asp Ile Lys Gln Leu His Glu Leu Arg Pro
195 200 205

Gly Leu Met Gly Trp Ile Leu Phe Asn Leu Ala Trp Thr Val Lys Gln
210 215 220

Tyr Asn Thr His Gly Phe Val Ser Asp Ser Ile Val Leu Val Asn Leu
225 230 235 240

Phe Glu Thr Trp Tyr Val Val Asp Ala Leu Trp Asn Glu Ser Lys Val
245 250 255

Leu Thr Thr Met Asp Ile Thr Thr Asp Gly Leu Gly Val Met Leu Leu
260 265 270

Phe Gly Asn Ala Val Trp Val Pro Phe Met Tyr Cys Leu Gln Ala Arg
275 280 285

Tyr Leu Ala Ser Phe Pro Val His Leu Gly Leu Leu Gly Ile Ala Gly
290 295 300

Val Leu Ala Val Gln Phe Thr Gly Tyr Ala Ile Phe Arg Gly Ala Asn
305 310 315 320

Asn Gln Lys Asn Ala Phe Arg Thr Asn Pro Ala Asp Pro Ala Val Ser
325 330 335

His Leu Lys Phe Met Thr Thr Lys Ser Gly Ser Lys Leu Leu Ile Ser
340 345 350

Gly Trp Trp Gly Val Ala Arg His Val Asn Tyr Phe Gly Asp Trp Ile
355 360 365

Met Ala Trp Ser Tyr Cys Leu Thr Thr Gly Phe Asn Thr Pro Leu Thr
370 375 380

Tyr Phe Tyr Val Ile Tyr Phe Gly Ile Leu Leu Leu His Arg Asp Arg
385 390 395 400

Arg Asp Glu Ala Lys Cys Arg Glu Lys Tyr Gly Lys Asp Trp Asp Arg
405 410 415

Tyr Cys Lys Val Val Lys Trp Arg Ile Ile Pro Gly Ile Tyr
420 425 430

<210> 10

<211> 365

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<212> PRT

<213> Arabidopsis thaliana

<400> 10

Met Asp Leu Gly Val Leu Leu Pro Ser Leu Gln Ser Val Tyr Val Leu
1 5 10 15Val Phe Tyr Phe Val Tyr Leu Ala Val Ala Gly Glu Ile Leu Pro Gly
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35 40 45Arg Cys Asn Gly Leu Leu Ala Leu Ile Leu Val Ala Ile Leu Gly
50 55 60Ile Cys Ala Lys Leu Gly Ile Val Ser Pro Leu Val Val Ala Asp Arg
65 70 75 80Gly Leu Glu Leu Leu Ser Ala Thr Phe Ile Phe Cys Val Leu Val Thr
85 90 95Leu Ala Leu Tyr Val Thr Gly Arg Ser Ser Ser Asn Lys Gly Ser Ser
100 105 110Leu Lys Pro His Val Ser Gly Asn Leu Val His Asp Trp Trp Phe Gly
115 120 125Ile Gln Leu Asn Pro Gln Phe Met Ser Ile Asp Leu Lys Phe Phe Phe
130 135 140Val Arg Ala Gly Met Met Gly Trp Leu Leu Ile Asn Leu Ser Ile Leu
145 150 155 160Ala Lys Ser Val Gln Asp Gly Ser Leu Ser Gln Ser Met Ile Leu Tyr
165 170 175Gln Ile Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe Val His Glu Glu
180 185 190Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg Leu Gly Phe Met
195 200 205Leu Val Phe Gly Asp Leu Leu Trp Ile Pro Phe Thr Phe Ser Ile Gln
210 215 220Gly Trp Trp Leu Leu His Asn Lys Val Glu Leu Thr Val Pro Ala Ile
225 230 235 240Val Val Asn Cys Leu Val Phe Leu Ile Gly Tyr Met Val Phe Arg Gly
245 250 255Ala Asn Lys Gln Lys His Ile Phe Lys Lys Asn Pro Lys Thr Pro Ile
260 265 270Trp Gly Lys Pro Pro Val Val Val Gly Gly Lys Leu Leu Val Ser Gly
275 280 285Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Met Leu
290 295 300Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser Pro Val Pro Tyr
305 310 315 320

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Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp Arg Glu Arg Arg
325 330 335

Asp Glu Val Arg Cys Ala Glu Lys Tyr Lys Glu Ile Trp Ala Glu Tyr
340 345 350

Leu Arg Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
355 360 365